

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2003, 22:38:40 ; Search time 12 Seconds
(without alignments)
1779.177 Million cell updates/sec

Title: US-10-098-602a-2

Perfect score: 2376
Sequence: 1 MTITYDELNLINRNGKIDTV.....INFSKQVTDWELNGFNRY 454

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	480.0	100.0	439	GLNA_THEMA	P36205 Thermotoga
2	466	19.6	443	GLNA_CLOSA	P10656 Clostridium
3	464	19.5	446	GLNA_LACIA	Q9cd19 Lactococcus
4	443	18.6	446	GLNA_METVO	P21154 methanococ
5	442.5	18.6	443	GLNA_BACSU	P12425 bacillus su
6	424.5	17.9	446	GLNA_STAMW	O59812 staphylococ
7	423	17.8	446	GLNA_STAMW	O99ug5 staphylococ
8	412	17.3	445	GLNA_LACDE	P45627 lactobacilli
9	411.5	17.3	443	GLNA_BACCE	P19064 bacillus ce
10	400.5	16.9	446	GLNA_METMP	O59648 methanococ
11	398.5	16.8	454	GLNA_METUA	O60182 methanococ
12	395	16.6	442	GLNA_METTH	O27612 methanobact
13	393.5	16.6	446	GLNA_METTH	O10378 mycobacteri
14	391	16.5	443	GLNA_PYRKO	O08467 pyrococcus
15	389.5	16.4	439	GLNA_PYRAB	Q9uy99 pyrococcus
16	389.5	16.4	439	GLNA_PYRAB	O05907 pyrococcus
17	387.5	16.3	454	GLNA_HALVO	P43386 halobacteri
18	386.5	16.3	454	GLNA_HALNI	O9nh12 halobacteri
19	386	16.2	491	GLNA_ARCFU	O29313 archaeoglob
20	381.5	16.1	439	GLNA_PYRMO	P36687 pyrococcus
21	376	15.8	443	GLNA_PYRMO	O58097 pyrococcus
22	353	14.9	435	GLNA_RHIME	O87393 rhizobium m
23	341	14.4	472	GLNA_RHIME	P78061 escherichia
24	330.5	13.9	469	GLNA_AQUAE	O66514 aquifex aeo
25	330	13.9	435	GLNA_RHILP	P31592 rhizobium l
26	327	13.8	471	GLNA_SULSO	P23794 sulfolobus
27	312	13.1	469	GLNA_STRRP	P73758 streptomyce
28	310.5	13.1	474	GLNA_ANASP	P00964 anabaena sp
29	308.5	13.0	474	GLNA_FRALP	P46033 frankia aln
30	303	12.8	478	GLNA_MYCTU	O10377 mycobacteri
31	302	12.7	470	GLNA_FREDI	P33335 firemycelia d
32	301	12.7	469	GLNA_STRVR	O05542 streptomyc
33	300.5	12.6	473	GLNA_SULAC	Q9hh09 sulfolobus

34	299	12.6	469	1	GLNA_STRCO	P15106 streptomyc
35	293	12.3	473	1	GLNA_SYNRP	P28605 synecchococ
36	287.5	12.1	469	1	GLNA_RHIME	O59747 rhizobium m
37	287	12.1	472	1	GLNA_HAEIN	P43794 haemophilus
38	283	11.9	468	1	GLNA_METCA	P15124 methylococ
39	283	11.9	472	1	GLNA_PASMU	O9c1p2 pasteurella
40	280	11.8	468	1	GLNA_AZOBK	P10583 azospirillum
41	278.5	11.7	468	1	GLNA_VIBAL	P19904 vibrio algi
42	276	11.6	467	1	GLNA_AZOCI	P22248 azotobacter
43	270	11.4	468	1	GLNA_AZOCI	P94126 azorhizobiu
44	269	11.3	481	1	GLNA_HELPY	P94845 helicobacte
45	267.5	11.3	469	1	GLNA_PROVU	P28786 proteus vul

ALIGNMENTS

RESULT 1
GLNA_THEMA STANDARD; PRT; 439 AA.
ID GLNA_THEMA
AC P36205;
DT 01-JUN-1994 (Rel. 29, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase) (GS).
GN GLNA OR TM0943.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=9226700; PubMed=1348781;
RA Sausgelandt A.M., Forlani G., Ambroselli F., Cammarano P., Tiboni O.;
RT "The glna gene of the extremely thermophilic eubacterium Thermotoga maritima: cloning, primary structure, and expression in Escherichia coli.";
RT J. Gen. Microbiol. 138:383-393(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=9287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A., McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.";
RT Nature 393:323-329(1999).
RL Nature 393:323-329(1999).
CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate + L-glutamine.
CC -1- SUBUNIT: Oligomer of 12 subunits arranged in the form of two hexagons (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ebi.ac.uk/announcements/ or send an email to license@ebi.ac.uk).
CC EMBL; X60160; CA42729.1; -
CC EMBL; AE001758; AAD36024.1; -
CC PIR; B72313; B72313.
CC HSSP; P06201; ILGR.
CC TIGR; TM0943; -
CC InterPro; IPR001691; GLN_synth.

downscaled

DR	InterPro: IPR004809; GlnA.		
DR	InterPro: IPR001637; GlnA adenyln.		
DR	Pfam; PF00120; gln-syntc_I.		
DR	Pfam; PF03951; gln-syntc_N; 1.		
DR	ProDom; PD001057; Gln_syntc_C; 1.		
DR	TIGRFAMs; TIGR00653; GlnA; 1.		
DR	PROSITE; PS00180; GlnA_1; 1.		
DR	PROSITE; PS00181; GlnA_ATP; 1.		
KW	Ligase; Complete proteome.		
KW	CONFLICT	204	204
FT	CONFLICT	280	A -> G (IN REF. 1).
FT	CONFLICT	336	A -> R (IN REF. 1).
FT	CONFLICT	336	S -> T (IN REF. 1).
SQ	SEQUENCE	439 AA; 50035 MW;	ABE3E674BD2F359 CRC64;

Query Match	20.2%;	Score 480;	DB 1;	Length 439;
Best Local Similarity	29.9%;	Pred. No. 1,1e-30;		
Matches 138;	Conservative 73;	Mismatches 209;	Indels 42;	Gaps 9;

Oy 3 TTYEDLNUNIRNGKIDTVDVLACVDMOGRMLKRLTGRHFLGDOCKLISTSTFYAVATIE 61
 Db 1 MTEITIKRIEENNAFIRLOFTDINGTL-----KOLEITPVFLESWED 45
 Oy 62 GIAGGGEYBIS-VDGTYSDDCHCADINSHTLLPWS-EGA-----VLAISPNHVTSTSEPL 114
 Db 46 GIMPDGSSIEGCVRIEESDMYLEKPVLDTPAVLFWTVDGAKSARVICDVTYR---DGKPF 101
 Oy 56 155 54
 115 FCSPEVILMOQLERLANLTKGLFASLEPNLENEYTKSASQCHMWKLNKTAOPHOHOMNI 174
 Db 102 EGDPRFLRMRMEKABOLGTYTPYAGEBMEGFILPINEKGEVDEFLD-----HGGFPLD 155
 Oy 175 SASGGIETMRSVRNKLEBAGIMEMTBEFLFESCHELNFVPADPLTMADRHIIAARGVR 234
 Db 156 LPLSKVEIRIDIALIEMKGIIVETHTHEVARSQSBVDRGYDTPLRTADNAQTVLVIK 215
 Oy 235 ENABOSGMVATPFAKLSSTRALGNACGITHSLDIAETBEKAFYONDNEYGSTIARWING 234
 Db 216 TMAIFGHYATHPKPPFYGVNDSGGMVHNSU--FRGDKNAFYDPDPLGSKELRFFVGG 273
 Oy 295 LTKYVEATFYEPFASINYSYKRLDPLTFAPFCOMALINDRTASAPLCSKSEGINVELRIG 354
 Db 274 ILKHAKALAAVNPNTINSYKRLDPLTFAPFCOMALINDRTASAPLCSKSEGINVELRIG 354
 Oy 355 GADLNDYLAFSATIIAAGISIEBEKLELPPFASGNVTI-----DKELPEFPNSLONATH 407
 Db 334 DPCSCNYILFAAIIAAGLGOIINKIEPFAVEENIYHMTSERBELNIESILPGSLKEAVE 339
 Oy 408 LKESKLNKTPGEKXILHYVNAANYEINEPSQVDMWENO 449
 Db 394 ELKQDVIIIDALGSHLPEKFVEAKDQKESFTYVIMMELOR 435

RESULT 2			
ID	GLNA_CLOSA	STANDARD;	PRT: 443 AA.
AC	P10656;		
DT	01-JUL-1989 (Rel. 11, Created)		
DT	01-JUL-1989 (Rel. 11, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase).		
GN	GLNA.		
OS	Clostridium saccharobutylicum.		
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;		
CC	Clostridium.		
OX	NCBI_TaxID=169679;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=P262;		
RX	MEDLINE=88086901; PubMed=2891680;		
RA	Janssen P.J., Jones W.A., Jones D.T., Woods D.R.;		
RT	"Molecular analysis and regulation of the glnA gene of the Gram-		
RL	positive anaerobe Clostridium acetobutylicum.",		
CC	Bacteriol. 170:400-408(1988).		
	-I- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate +		